

CC invention can be used in research; as nutritional supplements; for cell
 CC proliferation; cell differentiation or cytokine activity or to induce the
 CC production of cytokines; for immune stimulating or suppressing activity
 CC i.e generation of antibodies; for haematopoiesis regulating activity; for
 CC tissue growth activity; for activin/inhibin activity; for
 CC chemotactic/chemokinetic activity; for haemostatic and thrombolytic
 CC activity; for receptor/ligand activity; for anti-inflammatory activity or
 CC for tumour inhibition activity
 CC
 SQ Sequence 164 AA;

Query Match 99.9%; Score 851; DB 2; Length 164;
 Best Local Similarity 99.4%; Pred. No. 1.5e-89;
 Matches 164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MASPHQEPKPDLLIEIFRLGHEHMAIYIGGYVHILAPPEYFGAGSSVFSVLSNAEV 60
 DB 1 MASPHQEPKPDLLIEIFRLGHEHMAIYIGGYVHILAPPEYFGAGSSVFSVLSNAEV 60

QY 61 KRRLIEDVVGCCYRVNNSLDHEYQRPVEVITSSAKENVGOMKXSTVSRNCEHFTQL 120
 DB 61 KRRLIEDVVGCCYRVNNSLDHEYQRPVEVITSSAKENVGOMKXSTVSRNCEHFTQL 120

QY 121 RYGSRCQVEKAKVEGVATATGILVAGCSFXIRRYOKKATA 164
 DB 121 RYGSRCQVEKAKVEGVATATGILVAGCSFXIRRYOKKATA 164

RESULT 2
 AAM29736
 ID AAM29736 standard; protein; 164 AA.

AC AAM29736;
 XX 10-NOV-1998 (first entry)

DE Human H-rev 107-like protein (HREV).

XX Human; H-rev 107-like protein; HREV; prevention; diagnosis; cancer;
 KM autoimmune disorder.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 154
 FT /label= unknown
 FT /note= "encoded by GNG"

XX MO9836063-A1.

XX 20-AUG-1998.

XX 10-FEB-1998; 98W0-US002537.

XX 14-FEB-1997; 97US-00801742.

XX (INCYT) INCYTE PHARM INC.

XX Bandman O, Goli SK;

XX WPI; 1998-457113/39.

XX N-PSDB; AAV47554.

XX Nucleic acid encoding novel human H-rev 107-like protein - useful for
 PT e.g. diagnosis, prevention and treatment of cancers or auto-immune
 PT disorders.

XX Claim 1; Page 41-42; 56pp; English.

XX The present sequence represents human H-rev 107-like protein (HREV). The
 CC HREV nucleic acid and protein can be used for the diagnosis, prevention
 CC or treatment of cancer or autoimmune disorders
 XX

SQ Sequence 164 AA;

Query Match 99.8%; Score 850; DB 2; Length 164;
 Best Local Similarity 100.0%; Pred. No. 2e-89;
 Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASPHQEPKPDLLIEIFRLGHEHMAIYIGGYVHILAPPEYFGAGSSVFSVLSNAEV 60
 DB 1 MASPHQEPKPDLLIEIFRLGHEHMAIYIGGYVHILAPPEYFGAGSSVFSVLSNAEV 60

QY 61 KRRLIEDVVGCCYRVNNSLDHEYQRPVEVITSSAKENVGOMKXSTVSRNCEHFTQL 120
 DB 61 KRRLIEDVVGCCYRVNNSLDHEYQRPVEVITSSAKENVGOMKXSTVSRNCEHFTQL 120

QY 121 RYGSRCQVEKAKVEGVATATGILVAGCSFXIRRYOKKATA 164
 DB 121 RYGSRCQVEKAKVEGVATATGILVAGCSFXIRRYOKKATA 164

RESULT 3
 AAM60726
 ID AAM60726 standard; protein; 164 AA.

AC AAM60726;
 XX 02-SEP-1998 (first entry)

DE Full length tazarotene inducible Gene-3 (TIG3) protein sequence.

XX Tazarotene inducible gene-3; TIG3; identification; compound; treatment;
 KM hyperproliferative skin disorder; psoriasis; acne; dysplasia; cancer.

XX Homo sapiens.

XX US5776687-A.

XX 07-JUL-1998.

XX 28-FEB-1997; 97US-00808303.

XX 28-FEB-1997; 97US-00808303.

XX (ALLR) ALLERGAN.

XX Disepio D, Nagpal S, Chandraratna RA;

XX WPI; 1998-398020/34.

XX N-PSDB; AAV36092.

XX Identifying agents for treating hyper-proliferative skin diseases - from
 PT ability to induce tazarotene inducible gene-3 mRNA in cultured skin
 PT cells.

XX Example 2; Col 29-32; 20pp; English.

XX The present sequence is encoded by the full length cDNA sequence of
 CC tazarotene inducible gene-3 (TIG3). The cDNA sequence was obtained by
 CC alignment and combination of sequences AAV36088 and AAV36091. The
 CC specification describes a method for identifying compounds suitable for
 CC treating hyperproliferative disorders of the skin. The method comprises
 CC analysing samples of untreated and treated cultures of skin cells for
 CC presence of RNA from the TIG3 gene. If the treated sample has a higher
 CC concentration of the RNA than the control, then the test compound is
 CC identified as suitable for use as a treatment. The method is used to
 CC identify compounds which are potentially useful for treating psoriasis,
 CC acne or a wide range of dysplasias and cancers
 CC

XX Sequence 164 AA;

Query Match 98.6%; Score 840; DB 2; Length 164;
 Best Local Similarity 98.2%; Pred. No. 2.8e-86;
 Matches 161; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2004, 10:51:49 ; Search time 21 Seconds

(without alignments)
751.210 Million cell updates/sec

Title: US-10-020-618-1

Perfect score: 852
Sequence: 1 MASPHQEPKRGDLEIFRLG.....ILVVAGCSFXIRRYOKKARA 164

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	423.5	49.7	160	2	S42794	p18H-rev 107 prote
2	102	12.0	159	2	B82470	H-REV 107-related
3	92	10.8	1737	2	A37491	hypothetical helic
4	87.5	10.3	191	2	T50306	hypothetical prote
5	83.5	9.8	510	2	T44810	conserved hypothet
6	80	9.4	510	2	H69893	conserved hypothet
7	79.5	9.3	867	2	G95843	conserved hypothet
8	77.5	9.1	157	2	H86741	conserved hypothet
9	77.5	9.0	230	2	AC2351	hypothetical prote
10	75.5	8.9	119	2	AC2351	hypothetical prote
11	75.5	8.8	400	2	S54642	probable secreted
12	75	8.7	715	2	G86239	glycine cleavage T
13	74.5	8.7	453	2	T29493	protein F20B24.6
14	74	8.6	671	2	A10809	hypothetical prote
15	73.5	8.6	337	2	AC2006	DNA ligase (NAD) (
16	72.5	8.5	720	2	T47221	hypothetical prote
17	72.5	8.5	281	2	S18245	replication licens
18	72	8.5	363	1	S44734	xylf protein - Pae
19	72	8.5	353	1	S44734	probable protein-t
20	72	8.5	749	2	G88535	protein B0523.1 (f
21	72	8.5	749	2	B86403	probable mutator-1
22	72	8.5	895	2	T02597	Mutator-like trans
23	72	8.5	1127	2	B86386	probable mutator-1
24	71.5	8.4	252	2	T14564	phage lambda-relat
25	71.5	8.4	270	2	F64050	glucosamine-6-phos
26	71.5	8.4	693	2	G82618	plus biogenesis p
27	71.5	8.4	964	2	E71460	probable outer mem
28	71.5	8.4	1115	2	T09403	integrin alpha cha
29	71.5	8.4	1115	2	T09433	integrin alpha cha

30	71	8.3	107	2	T27713	hypothetical prote
31	71	8.3	129	2	G67615	conserved hypothet
32	71	8.3	553	2	A82513	methy-accepting c
33	71	8.3	556	2	T47552	hypothetical prote
34	71	8.3	669	2	JC5662	hepatoma-derived g
35	71	8.3	1286	1	S38058	hypothetical prote
36	70.5	8.3	293	2	S66356	mannose/glucose-bi
37	70.5	8.3	447	2	S32879	lipa protein - Nei
38	70.5	8.3	647	2	S61973	hypothetical prote
39	70.5	8.3	671	2	G91039	DNA ligase [import
40	70.5	8.3	671	2	F85863	DNA ligase [import
41	70.5	8.3	690	2	S28222	peroxidase (EC 1.1
42	70	8.2	621	2	E90253	formate hydroxylase
43	70	8.2	702	2	A96959	oxygen-sensitive r
44	70	8.2	5032	1	A35041	ryanodine receptor
45	70	8.2	5035	1	T46646	ryanodine receptor

ALIGNMENTS

RESULT 1

S42794
p18H-rev 107 protein - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999

C/Accession: S42794
R/Schaefer, R.

submitted to the EMBL Data Library, November 1993

A/Reference number: S42794

A/Accession: S42794

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-160 <SCH>

A/Cross-references: EMBL:X76453; NID:G433962; PIDN:CAAF5991.1; PID:G433963

Query Match

Best Local Similarity 49.7%; Score 423.5; DB 2; Length 160;

Matches 83; Conservative 24; Mismatches 50; Indels 1; Gaps 1;

QY	4	PHOEKPGDLEIFRLGVEHWALYIGDYVTHLAPSEYVPGAGSSVFSVLSNGAEVRE	63
DB	2	PIPEKPGDLEIFRPMXSHWAIYVGDGYVTHLAPPEIIPAGAAISALTDALYKE	61
QY	64	RLEDVGGCCYRVNNSLDHEYOQPPVEYIISAKEMGQKKKISVSRNCHFTQLRYG	123
DB	62	LIRDVAGDKYQVNNKDKETPLPKKIIPRAELVGOEVLRLTSENCHFVNEELRYG	121
QY	124	KSRQVEKAVEGVATAGILVVAGCSFXIRRYOKK	161
DB	122	VPRSDQV-RDITVKAIVTGVGLALGLGWLSNKQ	158

RESULT 2

B82470
H-REV 107-related protein VCA0346 [imported] - Vibrio cholerae (strain N16961 serogroup C

C/Species: Vibrio cholerae

C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C/Accession: B82470

R/Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;

Chadson, D.; Ermolaeva, M.D.; Vamthavanan, J.; Bass, S.; Qin, H.; Dragoti, I.; Sellers, P.

1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A/Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A/Reference number: A82035; MUID:20406833; PMID:10952301

A/Accession: B82470

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-159 <HEI>

A/Cross-references: GB:AE004372; GB:AE003853; NID:G9657741; PIDN:AAFP6254.1; GSPDB:GN001;

A/Experimental source: serogroup O1, strain N16961; biotype El Tor

A/Genes: VCA0346

A:Map position: 2

Query Match 12.0%; Score 102; DB 2; Length 159;
 Best Local Similarity 25.4%; Pred. No. 0.013;
 Matches 43; Conservative 19; Mismatches 59; Indels 48; Gaps 9;

QY 6 QEPKPGDLIFRLG-YEHWALYIGGYVHLAPSEYPGAGSSVFSVLSNAEKYRER 64
 DB 4 QNNAQDGV-VSNFGVYQWMSL-VSDLLC-----EKGLPMILSLTORNGVQEST 51

QY 65 LEDVVGCCCYRVNNSLDHEX-----QRPYEVIISSAKEMVGQKMKYSIVSRNCEHFV-- 117
 DB 52 MDVVTQC-----KHATPAKYTDPRPYSEVLELARSQIG-TMKYSLTDNRCEHFVVM 101

QY 118 -----TOLRYGKSKC-----KQYERAKYEVYATMLGLTVY 148
 DB 102 ATGLKRSITQVIGATGATGAVLGSVLGVISENPKFAKFLGALALGSLAV 150

RESULT 3

A37491

hypothetical helicase/polymerase polypeptide - Southampton virus

N:Alternate names: orf1 protein

C:Species: Southampton virus

C>Date: 03-Mar-1994 #sequence_revision 25-Apr-1997 #text_change 17-Mar-2000

C:Accession: A37491

R:Lambden, P. R.; Gaul, E. O.; Ashley, C. R.; Clarke, I. N.

Science 259, 516-519, 1993

A:Title: Sequence and genome organization of a human small round-structured (Norwalk-like

A:Reference number: A37491; PMID:9312023; PMID:9380940

A:Contents: Small round-structured virus, SRV, Norwalk virus, Norwalk-like virus, serot

A:Accession: A37491

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: genomic RNA

A:Residues: 1-1737 <LAMB>

A:Note: sequence extracted from NCBI backbone (NCBI:123456)

C:Superfamily: rabbit calicivirus RNA-directed RNA polymerase

Query Match 10.8%; Score 92; DB 2; Length 1737;
 Best Local Similarity 24.6%; Pred. No. 2;
 Matches 29; Conservative 20; Mismatches 45; Indels 24; Gaps 5;

QY 4 PHQPKRGLIEFRLGYEHMALYIGGYVHLAPSEYPGAGSSVFSVLSNAEKYR 63
 DB 137 PASEPTIGDIEFEGHITRYIYIGQKTVGHSP-----QAFFS-----VARV 181

QY 64 RLEDVVGCCCYRVNNSLDHEYOPRV-EVLISSAKEMVGQKMKYSIVSRNCEHFV 120
 DB 182 TIQPI--AAWWRVC-----YIPQKRLSYDQLKELENEPMPYALITNNCFEFCOV 231

RESULT 4

T50306

hypothetical protein SPAPYU7.06 [imported] - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000

C:Accession: T50306

R:McDougal, R. C.; Rajandream, M. A.; Bartell, B. G.; Saunders, D.; Harris, D.

submitted to the EMBL Data Library, January 2000

A:Reference number: Z25059

A:Accession: T50306

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-191 <MCD>

A:Cross-references: EMBL:AL136521; PIDN:CA866315.1; GSPDB:GN00066; SPDB:SPAPYU7.06

A:Experimental source: strain 972H(-); clone plasmid pYU7

C:Genetics:

A:Gene: SPDB:SPAPYU7.06

A:Map position: 1

Query Match 10.3%; Score 87.5; DB 2; Length 191;
 Best Local Similarity 31.0%; Pred. No. 0.43;
 Matches 31; Conservative 17; Mismatches 33; Indels 19; Gaps 6;

QY 24 WALYIGGYVHLAPSEYR-GA---GSSSVFSVLSNAEKYRERLEDVVGCCCYRVN 78
 DB 11 WTLIDGIVHGLVLEGKFAFAHIEPGSTGVF-----ATMRPPLP-----GCRWCSI 60

QY 79 SLDEYOPRV--VEVISSAKEMVGQKMKYSIVSRNCEHF 116
 DB 61 ALPNCTLPKPDVRIILRLSQEPFG--LSYSLERKCNHF 98

RESULT 5

T44810

conserved hypothetical protein ymgk [imported] - Bacillus subtilis

C:Species: Bacillus subtilis

C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 28-Jul-2000

C:Accession: T44810

R:Dultman, E. H.; Hamcen, L. W.; Rembold, M.; Venema, G.; Seltz, H.; Saenger, W.; Bernhard

Proc. Natl. Acad. Sci. U.S.A. 96, 13294-13299, 1999

A:Title: The mycosubtilin synthetase of Bacillus subtilis ATCC6633: A multifunctional hy

A:Reference number: Z22648; PMID:20027541; PMID:10557314

A:Accession: T44810

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-510 <DUIT>

A:Cross-references: EMBL:AF184956; NID:96449053; PIDN:AA08799.1; PID:96449059

A:Experimental source: strain ATCC6633

C:Genetics:

A:Gene: ymgk

C:Superfamily: conserved hypothetical protein ymgk

Query Match 9.8%; Score 83.5; DB 2; Length 510;
 Best Local Similarity 25.0%; Pred. No. 3.3;
 Matches 29; Conservative 25; Mismatches 41; Indels 21; Gaps 6;

QY 23 HMALYIGGYVHLAPSEYRPGAGSSVFSVLSN--SAEYKRELEDDVVGCCCYRVN 80
 DB 294 HW---IQEGDIDYIAFQIYVSGNAAAYDLADWNEKRNKPNVHYIGQAAVKINNPF 350

QY 81 D-----HEYQPREVEIISSAKEMVGQKMKYSIVSRNCEHF-----VTOLRYGK 124
 DB 351 DPFMSDEBYR---QITLNQLELVKSGMVFSLKDKNKNPFIKORLITEL-YSK 402

RESULT 6

H69893

conserved hypothetical protein ymgk - Bacillus subtilis

C:Species: Bacillus subtilis

C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 28-Jul-2000

C:Accession: H69893

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A. M.; Alloni, G.; Azevedo, V.; Berta

C.; Bron, S.; Brouillet, S.; Brusch, C. V.; Caldwell, B.; Capuano, V.; Carter, N. M.; Cho

A.; Ehrlich, S. D.; Emerson, P. T.; Ertian, K. D.; Berrington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Gall

lecher, U.; Harwood, C. R.; Henaut, A.; Hilbert, H.; Holappel, S.; Hosono, S.; Hullo, M. F.

Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lardinois, S.; Maue

V. M.; Ogawa, K.; Ogilwara, A.; Onodera, B.; Park, S. H.; Parro, V.; Pohl, T. M.; Portetel

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sekiguchi, J.; Sekowska, A.; Ser

A:Authors: Schleich, S.; Schroeder, R.; Seifert, F.; Sekiguchi, J.; Sekowska, A.; Ser

A.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K

A:Authors: Yoshikawa, H. F.; Zundstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A:Reference number: A69580; PMID:98044033; PMID:9384377

A:Accession: H69893

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-510 <KUN>

A:Cross-references: GB:Z59113; GB:AL009126; NID:92634090; PIDN:CA813711.1; PID:92634211

A:Experimental source: strain 168

C:Genetics:

A:Gene: ymgk

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2004, 10:48:44 ; Search time 18 Seconds

(Without alignments)
474.417 Million cell updates/sec

Title: US-10-020-618-1

Perfect score: 852
Sequence: 1 MASPHQEPKPGDLIEIFRLG.....ILVAGCSFIRRYQKAKA 164

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	851	99.9	164	1	TIG3_HUMAN
2	423.5	49.7	160	1	HRS3_RAT
3	418.5	49.1	162	1	HRS3_HUMAN
4	407.5	47.8	162	1	HRS2_HUMAN
5	382	44.8	270	1	HRS2_MOUSE
6	380	44.6	279	1	HRS1_HUMAN
7	350	41.1	168	1	HRS1_MOUSE
8	332.5	39.0	167	1	HRS1_MOUSE
9	92	10.8	1788	1	POLN_SOUTV3
10	77	9.0	400	1	GCST_YEAST
11	75	8.8	458	1	GCST_YEAST
12	72.5	8.5	397	1	YGO1_HUMAN
13	72.5	8.5	720	1	MCW7_XENLA
14	72	8.5	281	1	XYLF_PSEPU
15	72	8.5	437	1	KI31_CAEEL
16	71.5	8.4	270	1	NAGB_HABIN
17	71.5	8.4	624	1	MUTL_XANCP
18	71.5	8.4	964	1	PMPE_CHLTR
19	71.5	8.4	1115	1	ITAS3_DROME
20	71	8.3	1286	1	KYV3_YEAST
21	70.5	8.3	293	1	LECI_CLAUT
22	70.5	8.3	647	1	NOGI_YEAST
23	70.5	8.3	690	1	PERO_DROME
24	70	8.2	5035	1	RYR1_PIG
25	70	8.2	5037	1	RYR1_RABIT
26	70	8.2	5038	1	RYR1_HUMAN
27	69.5	8.2	377	1	TDP_DROME
28	69.5	8.2	305	1	PKA1_TRYB
29	69.5	8.2	3178	1	Y89_CAEEL
30	69	8.1	320	1	DEPA4_BPER6
31	69	8.1	348	1	N33_HUMAN
32	69	8.1	705	1	RNR_AQUAE
33	68.5	8.0	406	1	METK_MERUA

34	68.5	8.0	632	1	SEAB_HUMAN
35	68.5	8.0	671	1	DNLJ_ECOLI
36	68	8.0	162	1	CYTX_ONCHO
37	68	8.0	697	1	AD26_MOUSE
38	67.5	7.9	249	1	HYUE_PSESN
39	67.5	7.9	5327	1	MACF_MOUSE
40	67	7.9	772	1	CADJ_HUMAN
41	66.5	7.8	217	1	MMCI_METAC
42	66.5	7.8	248	1	KAD_GALA
43	66.5	7.8	292	1	DHII_SHEEP
44	66.5	7.8	359	1	MTD_FRAN
45	66.5	7.8	444	1	HSLD_HAETN

ALIGNMENTS

RESULT 1
TIG3_HUMAN STANDARD; PRT; 164 AA.
AC Q9UL19; O95200;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Retinoid acid receptor responder protein 3 (Tazartene-induced gene 3 protein) (RAR-responsive protein TIG3) (Retinoid inducible gene 1 protein).
GN RARRES3 OR TIG3 OR RIGL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.
NCBI_Taxid=9606;
RX MEDLINE=9061949; PubMed=9843971;
RA Disseplo D., Ghosh C., Eckert R.L., Deucher A., Robinson N., Duvic M., Chandraratna R.A.S., Nagpal S.;
RT "Identification and characterization of a retinoid-induced class II tumor suppressor/growth regulatory gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:14811-14815 (1998).
RN [3]
RP SEQUENCE FROM N.A.
RQ Kato S.;
RN Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
RC [4]
RX TISSUE=Lung;
RA MEDLINE=22388257; PubMed=12477932;
RA Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Kiansner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buertow K.H., Schaefer C.F., Bat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M., Ueda T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loguillano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W., Villalón D.K., Muzny D.M., Sodergren E.D., Lu X., Gibbs R.A., Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Rutherford J.Y.S.N., Krzywinski M.I., Skalska D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

```

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: May be a growth regulator that mediates some of the
CC growth suppressive effects of retinoids.
CC -1- TISSUE SPECIFICITY: Expressed in many tissues. Not expressed in
CC heart, brain, and testis.
CC -1- INDUCTION: By tazarotene.
CC -1- SIMILARITY: Belongs to the H-rev107 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF092922; AAF02294.1; -
DR EMBL; AF060228; AAC84000.1; -
DR EMBL; AB030815; BAB08109.1; -
DR EMBL; BC009678; AAH09678.1; -
DR Genbank; HGNC:9869; RAREB53.
DR MIM; 605092; -
DR InterPro; IPR007053; NC.
DR Pfam; PF04970; NC; 1.
FT CONFLICT 63 E -> G (IN REF. 2).
FT CONFLICT 118 T -> A (IN REF. 2).
SQ SEQUENCE 164 AA; 18179 MW; 956258BFD375FD38 CRC64;

Query Match 99.9%; Score 851; DB 1; Length 164;
Best Local Similarity 99.4%; Pred. No. 3.5e-77;
Matches 163; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSPHPEPPGDLIEFRFGYEHMALYIGDGYVHILAPSEYFGAGSSVFSVLSNAEY 60
DB 1 MSPHPEPPGDLIEFRFGYEHMALYIGDGYVHILAPSEYFGAGSSVFSVLSNAEY 60
QY 61 KSERLEDVVGCCCYRVNNSLDHEYOPRPEVVIISAKENVGQMKXSYVSRNCEHFVTL 120
DB 61 KSERLEDVVGCCCYRVNNSLDHEYOPRPEVVIISAKENVGQMKXSYVSRNCEHFVTL 120
QY 121 RYKSKRCQYERAKYEVGATALGLIVAGCSFXIRRYOKKATA 164
DB 121 RYKSKRCQYERAKYEVGATALGLIVAGCSFXIRRYOKKATA 164

RESULT 2
HRS3 RAT STANDARD; PRT; 160 AA.
AC P53817;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE HRS-1-like suppressor 3 (H-rev 107 protein).
GN HRS1S3 OR HREV107 OR H-REV107.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=94119589; PubMed=8290259;
RA Hajnal A.; Klemenz R.; Schaefer R.;
RT "Subtraction cloning of H-rev107, a gene specifically expressed in
RT H-ras resistant fibroblasts."
RL Oncogene 9:479-490(1994).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC AND ALSO IN CELL MEMBRANES.
CC -1- SIMILARITY: Belongs to the H-rev107 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X76453; CAAS5991.1; -
DR PIR; S42794; S42794.
DR InterPro; IPR007053; NC.
DR Pfam; PF04970; NC; 1.
SQ SEQUENCE 160 AA; 17778 MW; A0B32D6FA0BD12E6 CRC64;

Query Match 49.7%; Score 423.5; DB 1; Length 160;
Best Local Similarity 52.5%; Pred. No. 7.6e-35;
Matches 83; Conservative 24; Mismatches 50; Indels 1; Gaps 1;

QY 4 PHQEPKPGDLIEFRFGYEHMALYIGDGYVHILAPSEYFGAGSSVFSVLSNAEYKRE 63
DB 2 PIPEPKPGDLIEFRFGYEHMALYIGDGYVHILAPSEYFGAGSAINALTDKALVKE 61
QY 64 RLEDVVGCCCYRVNNSLDHEYOPRPEVVIISAKENVGQMKXSYVSRNCEHFVTLRG 123
DB 62 LRDVVGKDKYQVNNHDXEYTPLPINKTIQRAEELVQGEVLYRLTSENCEHFVNLRYG 121
QY 124 KSRCKQYERAKYEVGATALGLIVAGCSFXIRRYOKK 161
DB 122 VPRSDVY-KDTYKATVTVGGLAALGLIVMLSRKQK 158

RESULT 3
HRS3 HUMAN STANDARD; PRT; 162 AA.
AC P53816; Q9HD01;
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE HRS-1-like suppressor 3 (H-rev 107 protein homolog) (HREV107-3).
GN Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98442971; PubMed=9771974;
RA Huemann K.; Sers C.; Fietze E.; Mincheva A.; Lichter P.; Schaefer R.;
RT "Transcriptional and translational downregulation of H-REV107, a class
RT II tumour suppressor gene located on human chromosome 11q11-12."
RL Oncogene 17:1105-1112(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Kato S.;
RL Submitted (AUG-1999) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Siegrist S.; Feral C.; Chami M.; Solhonne B.; Rajpert-De Meyts E.;
RA Gueliaen G.; Bulle F.;
RT "Homo sapiens testis HREV107-3 mRNA."
RL Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=23388257; PubMed=12477932;
RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;
RA Klausner R.D.; Collins F.S.; Wagner L.; Shennan C.M.; Schuler G.D.;
RA Altschul S.F.; Zeeberg B.; Buettow K.H.; Schaefer C.F.; Bhat N.K.;
RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.;
RA Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.;
RA Siegelman M.; Soares M.B.; Donald M.F.; Casavant T.L.; Scheetz T.E.;
RA Brownstein M.J.; Udell T.B.; Toshiyuki S.; Carninci P.; Prange C.;
RA Rana S.S.; Loggellano N.A.; Peters G.J.; Abramson R.D.; Millar S.J.;
RA Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;
RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Huiyk S.W.;

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OM protein - protein search, using sw model

Run on: March 31, 2004, 10:50:09 ; Search time 42 Seconds
(without alignments)
1232.023 Million cell updates/sec

Title: US-10-020-618-1
Perfect score: 852
Sequence: 1 MSPHQEPKPGDLIEIFRLG.....ILVAGCSFXIRRYOKKATA 164

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriapi:*
- 17: sp_archaeapi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	411.5	48.3	162	11	Q8R3U1
2	390.5	45.8	168	11	Q8BWF7
3	380	44.6	268	4	Q8NB88
4	345	40.5	168	4	Q8BWS9
5	258.5	30.3	235	5	Q8T778
6	150.5	17.7	231	11	Q9J161
7	146.5	17.2	230	4	Q9S237
8	146.5	17.2	230	4	Q8N716
9	146.5	17.2	230	6	Q9BGI2
10	146.5	17.2	231	11	Q9YI60
11	136	16.0	310	4	Q96KX1
12	127.5	15.0	292	4	Q8TAM5
13	125	14.7	240	16	Q8EGZ0
14	123.5	14.5	292	4	Q96KX4
15	123.5	14.5	292	4	Q8UJ22
16	122.5	14.4	292	11	Q9D650

17	121.5	14.3	292	11	Q99X34	Q99K34	mus musculus
18	115.5	13.6	2134	12	Q9YLS4	Q9YLS4	avian enceph
19	108	12.7	227	16	Q7V994	Q7V994	prochloroto
20	102	12.0	159	16	Q9KMU7	Q9KMU7	vibrio chol
21	98	11.5	1789	12	Q83883	Q83883	normal vir
22	97	11.4	260	10	Q8LBP8	Q8LBP8	arabidopsis
23	96	11.3	199	16	Q8EDP8	Q8EDP8	shewanella
24	95	11.2	259	10	Q9JVS1	Q9JVS1	arabidopsis
25	94.5	11.1	242	10	Q9FPF0	Q9FPF0	arabidopsis
26	93.5	11.0	283	10	Q9FEF7	Q9FEF7	arabidopsis
27	92.5	10.9	212	16	Q7UA38	Q7UA38	synchococ
28	92	10.8	1788	12	Q8JVV6	Q8JVV6	normal vir
29	91	10.7	1787	12	Q8JXJ1	Q8JXJ1	normal vir
30	89	10.4	1785	12	Q9DU47	Q9DU47	chiba virus
31	87.5	10.3	201	3	Q8X1T0	Q8X1T0	schizosac
32	86.5	10.2	398	16	Q9KY68	Q9KY68	strepcomyc
33	85	10.0	1699	12	Q8UX16	Q8UX16	normal vir
34	83.5	9.8	337	16	Q8ZAU4	Q8ZAU4	strepcomyc
35	83.5	9.8	510	2	Q9R917	Q9R917	bacillus su
36	83	9.7	358	16	Q8ZHP1	Q8ZHP1	strepcomyc
37	82.5	9.7	252	10	Q8LSG9	Q8LSG9	arabidopsis
38	82.5	9.7	252	10	Q9M672	Q9M672	arabidopsis
39	82	9.6	347	16	Q9KY71	Q9KY71	strepcomyc
40	81.5	9.6	2256	12	Q8UJ19	Q8UJ19	ljungan vir
41	81	9.5	1784	12	Q9Y515	Q9Y515	normal vir
42	80	9.4	510	16	Q35015	Q35015	bacillus su
43	79.5	9.3	847	16	Q92X67	Q92X67	rhizobium m
44	79.5	9.3	2253	12	Q8JY20	Q8JY20	ljungan vir
45	79	9.3	1697	12	Q8JUL0	Q8JUL0	normal vir

ALIGNMENTS

RESULT 1
ID Q8R3U1 PRELIMINARY: PRT: 162 AA.
AC Q8R3U1
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to HRAS-like suppressor 3.
GN HRASLS3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC024581: AAH24581.1;
DR MGD; MGI:2179715; Hras183.
DR InterPro, IPR007053; NC.
DR Pfam, PF04970; NC; 1.
SQ SEQUENCE 162 AA; 17858 MW; EB180D8CF00AB2AB CRC64;

Query Match 48.3%; Score 411.5; DB 11; Length 162;
Best Local Similarity 51.9%; Pred. No. 6.8e-35;
Matches 84; Conservative 21; Mismatches 56; Indels 1; Gaps 1;
QY 1 MSPHQEPKPGDLIEIFRLGYEHMALYTGQYVHLAPSSYPGAGSSVPSVLSNAEV 60
1 MLAPPEPKPGDLIEIFRPMYRHWAIYVGDGYVHLAPSSVAGAGASINSALTDKAIV 60
DB 61 KRERLDGVGGCCVRVNNSLDHEYQRPVEVYISAKEMGQKKKYSIVSNSEHFVQL 120
61 KKEILCHVAGKDKQVANKHDEFTPLSKTIQRAELVQGEVYIRLTSNCEHFVNEI 120
QY 121 RYKSKRCQVAKAYGVGA-TALGILVAGCSFXIRRYOKK 161
121 RYGVPRSDQVRDAVAVGIALGVLGVMLSRNKKQKQ 162

RESULT 2

Q8BWF7 08BWF7 PRELIMINARY; PRT; 168 AA.
 AC Q8BWF7;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE H-REV 107 protein homolog.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium.
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 DR EMBL: AK052657; BAC35085.1; --
 DR InterPro: IPR007053; NC.
 DR Pfam: PF04970; NC; 1.
 SQ SEQUENCE 168 AA; 18932 MW; 73F410B7F832256 CRC64;

Query Match 45.8%; Score 390.5; DB 11; Length 168;
 Best Local Similarity 53.3%; Pred. No. 1,1e-32;
 Matches 81; Conservative 20; Mismatches 48; Indels 3; Gaps 2;

QY 1 MASPQPPKGGDIEIFRLGYEHMALYIGDGYVTHLAPSEYPGAGSSVSFVLSNAGV 60
 DB 1 MAPRIEPPKGGDIEIFRPMYRHMALYVGDGYVTHLAPSEYAGAGASIMGALTDKALV 60
 QY 61 KRERLDVVGGCCYRVNNSLDHEYQPRPVEVIISAKEMVQKKKYSIVRNCHEFTQL 120
 DB 61 KRELLCHVAGKDKYQVNNHDEYTPLPSTKIIGKRLRVLGVEVLYRLSRNCHEFTVNL 120
 QY 121 RYKSKRCQY--EKAVVEGVATALGILVAG 150
 DB 121 RYGVPRSDQYCHRPCTLTIGV--RSFSQLPVG 151

RESULT 3

Q8NEB8 08NEB8 PRELIMINARY; PRT; 269 AA.
 AC Q8NEB8;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Similar to H-rev107-like protein 5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Strausberg R.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC034222; AA034222.1; --
 DR InterPro: IPR007053; NC.
 DR Pfam: PF04970; NC; 1.
 SQ SEQUENCE 269 AA; 29257 MW; 2018B203C2BFC9B CRC64;

Query Match 44.6%; Score 380; DB 4; Length 269;
 Best Local Similarity 54.2%; Pred. No. 2,6e-31;
 Matches 77; Conservative 21; Mismatches 40; Indels 4; Gaps 2;

QY 8 PKFGDIEIFRLGYEHMALYIGDGYVTHLAPSEYPGAGSSVSFVLSNAGVKKERLED 67
 DB 120 PRFGDIEIFRLGYEHMALYVDDCVHLAPSEYEVG--SITISFRAVAVKTSRLD 177

QY 68 VVGGCCYRVNNSLDHEYQPRPVEVIISAKEMVQKKKYSIVRNCHEFTQLRYGKRC 127

DB 178 VLVGCSMKVNNKDKDGLTLPVVDITLQRTKMNKVIQVSLIGNCBHFVNGLRVGPFS 237

QY 128 KOYEKAVEGVATALGILVVA 149

DB 238 QVEVHALME--GAKAAGAVISA 257

RESULT 4

Q86WS9 086WS9 PRELIMINARY; PRT; 168 AA.
 AC Q86WS9;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE HRAS-like suppressor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Strausberg R.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC048095; AA048095.1; --
 DR InterPro: IPR007053; NC.
 DR Pfam: PF04970; NC; 1.
 SQ SEQUENCE 168 AA; 18751 MW; 1184423034D8B39B CRC64;

Query Match 40.5%; Score 345; DB 4; Length 168;
 Best Local Similarity 49.0%; Pred. No. 6,4e-28;
 Matches 71; Conservative 24; Mismatches 42; Indels 8; Gaps 2;

QY 8 PKFGDIEIFRLGYEHMALYIGDGYVTHLAPSEYPGAGSSVSFVLSNAGVKKERLED 67
 DB 15 PCFGDIEIFRPPYQHMALYIGDGYVINIAPVDGIP--ASTSKASVSSQALYKMQLLKD 73
 QY 68 VVGGCCYRVNNSLDHEYQPRPVEVIISAKEMVQKKKYSIVRNCHEFTQLRYGKRC 127
 DB 74 VVGNDFYRINKKVDETPLPVEEIIKRSSEFVIGEVAYVILVNDDEHFTLLRYGEGVS 133
 QY 128 KO-----VEKAVEGVATALGI 145
 DB 134 EQANRAISTVEFTAAVGFSPGL 158

RESULT 5

Q8T778 08T778 PRELIMINARY; PRT; 235 AA.
 AC Q8T778;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Branchiostoma floridae (Florida lancelet) (Amphioxus).
 OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
 OC Branchiostoma.
 OX NCBI_TaxID=7739;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=11967531;
 RA Abi-Rached L., Gilles A., Shiina T., Pontarotti P., Inoko H.;
 RT "Evidence of an bloc duplication in vertebrate genomes."
 RL Nat. Genet. 0:0-0(2002).
 DR EMBL: AF391288; AA018866.1; --
 DR InterPro: IPR007053; NC.
 DR Pfam: PF04970; NC; 1.
 KV Hypothetical protein.
 SQ SEQUENCE 235 AA; 27172 MW; D88AC7DE1E1F5FC8 CRC64;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2004, 10:55:44 ; Search time 22 Seconds
(Without alignments)
384.848 Million cell updates/sec

Title: US-10-020-618-1

Perfect score: 852
Sequence: 1 MASPHQEPKPGDLIEIFRLG.....ILVAGCSFYIRRYQKATA 164

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCITUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	850	99.8	164	US-08-801-742-1	Sequence 1, Appl1
2	840	98.6	164	US-08-808-303-8	Sequence 8, Appl1
3	840	98.6	164	US-08-996-533-8	Sequence 8, Appl1
4	839	98.5	164	US-08-808-303-12	Sequence 12, Appl1
5	839	98.5	164	US-08-996-533-12	Sequence 12, Appl1
6	623	73.1	124	US-08-808-303-3	Sequence 3, Appl1
7	623	73.1	124	US-08-996-533-3	Sequence 3, Appl1
8	423.5	49.7	160	US-08-801-742-4	Sequence 4, Appl1
9	417.5	49.0	162	US-08-801-742-3	Sequence 3, Appl1
10	98	11.5	1738	US-08-486-049-2	Sequence 2, Appl1
11	85.5	10.0	212	US-09-328-352-6684	Sequence 6684, Ap
12	72.5	8.5	462	US-09-328-352-7128	Sequence 7128, Ap
13	71.5	8.4	674	US-09-489-039A-9158	Sequence 9158, Ap
14	71.5	8.4	964	US-09-556-877-177	Sequence 177, App
15	71.5	8.4	964	US-08-620-412C-177	Sequence 177, App
16	71.5	8.4	964	US-09-598-419-177	Sequence 177, App
17	71.5	8.4	977	US-09-556-877-191	Sequence 191, App
18	71.5	8.4	977	US-09-620-412C-191	Sequence 191, App
19	71.5	8.4	977	US-09-598-419-191	Sequence 191, App
20	70	8.3	235	US-08-760-745-1	Sequence 1, Appl1
21	70	8.2	287	US-09-105-697-7	Sequence 7, Appl1
22	70	8.2	830	US-07-977-434-6	Sequence 6, Appl1
23	70	8.2	830	US-08-458-819-6	Sequence 6, Appl1
24	70	8.2	830	PCT-US91-07035-6	Sequence 6, Appl1
25	69	8.1	347	US-08-445-515-56	Sequence 56, Appl1
26	69	8.1	348	US-08-445-515-56	Sequence 56, Appl1
27	68.5	8.0	599	US-09-252-991A-19543	Sequence 19543, A

28	68.5	8.0	632	1	US-08-295-814E-10	Sequence 10, Appl1
29	68.5	8.0	632	3	US-09-343-361-10	Sequence 10, Appl1
30	68.5	8.0	632	5	PCT-US93-01959-10	Sequence 10, Appl1
31	68.5	8.0	671	4	US-09-708-426-11	Sequence 11, Appl1
32	68.5	8.0	916	4	US-09-688-078-9	Sequence 9, Appl1
33	68	8.0	162	4	US-08-849-303-25	Sequence 25, Appl1
34	68	8.0	234	4	US-09-800-729-150	Sequence 150, App
35	68	8.0	452	4	US-09-489-039A-11013	Sequence 11013, A
36	68	8.0	525	1	US-08-298-426-4	Sequence 4, Appl1
37	67.5	7.9	179	4	US-09-489-039A-9458	Sequence 9458, Ap
38	67	7.9	287	3	US-09-105-697-8	Sequence 8, Appl1
39	67	7.9	379	4	US-09-489-039A-11814	Sequence 11814, A
40	66.5	7.8	160	4	US-09-107-532A-7249	Sequence 7249, Ap
41	66.5	7.8	230	4	US-09-328-352-7052	Sequence 7052, Ap
42	66.5	7.8	501	2	US-08-408-095-31	Sequence 31, Appl1
43	66.5	7.8	969	2	US-08-548-159-1	Sequence 1, Appl1
44	66.5	7.8	986	2	US-08-548-159-3	Sequence 3, Appl1
45	66.5	7.8	2391	2	US-08-446-855A-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-08-801-742-1
Sequence 1, Application US/08801742

Patent No. 6359123

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

TITLE OF INVENTION: A NOVEL H-REV107-LIKE

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS: Proteins

ADDRESS: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/801,742

FILING DATE: Filed Herewith

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy U.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0200 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166

INFORMATION FOR SEQ. ID NO. 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 164 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-801-742-1

Query Match

Best Local Similarity 99.8%; Score 850; DB 4; Length 164;

Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MASPHQEPKPGDLIEIFRLG.....ILVAGCSFYIRRYQKATA 164

DB 1 MASPHQEPKPGDLIEIFRLGYEHMALYIGDGYVHILAPSEYFGAGSSVFSVLSNSAEV 60
QY 61 KRERLDGVGGCCYRVNNSLDHEYOPRPEVITISSAKEMVGOMKXYSIVSRNCEHFTVTL 120
DB 61 KRERLDGVGGCCYRVNNSLDHEYOPRPEVITISSAKEMVGOMKXYSIVSRNCEHFTVTL 120
QY 121 RYKSRCKQVEKAKVEGVATAGILVAGCSFXIRRYOKKATA 164
DB 121 RYKSRCKQVEKAKVEGVATAGILVAGCSFXIRRYOKKATA 164

RESULT 2
US-08-808-303-8
Sequence 8, Application US/08808303
Patent No. 5776687
GENERAL INFORMATION:
APPLICANT: Nagpal, Sunil
APPLICANT: Chandraratna, Roshantha
TITLE OF INVENTION: RETINOID INDUCED GENE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,303
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: ALRGN.062A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 164 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-808-303-8

Query Match 98.6%; Score 840; DB 1; Length 164;
Best Local Similarity 98.2%; Pred. No. 3.2e-93;
Matches 161; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

DB 1 MASPHQEPKPGDLIEIFRLGYEHMALYIGDGYVHILAPSEYFGAGSSVFSVLSNSAEV 60
QY 61 KRERLDGVGGCCYRVNNSLDHEYOPRPEVITISSAKEMVGOMKXYSIVSRNCEHFTVTL 120
DB 61 KRERLDGVGGCCYRVNNSLDHEYOPRPEVITISSAKEMVGOMKXYSIVSRNCEHFTVTL 120
QY 121 RYKSRCKQVEKAKVEGVATAGILVAGCSFXIRRYOKKATA 164
DB 121 RYKSRCKQVEKAKVEGVATAGILVAGCSFXIRRYOKKATA 164

RESULT 3
US-08-996-533-8
Sequence 8, Application US/08996533
Patent No. 6294657
GENERAL INFORMATION:
APPLICANT: Nagpal, Sunil
APPLICANT: Disepio, Daniel
APPLICANT: Chandraratna, Roshantha
TITLE OF INVENTION: RETINOID INDUCED GENE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,533
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/808,303
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: ALRGN.062A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 164 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-996-533-8

Query Match 98.6%; Score 840; DB 3; Length 164;
Best Local Similarity 98.2%; Pred. No. 3.2e-93;
Matches 161; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

DB 1 MASPHQEPKPGDLIEIFRLGYEHMALYIGDGYVHILAPSEYFGAGSSVFSVLSNSAEV 60
QY 61 KRERLDGVGGCCYRVNNSLDHEYOPRPEVITISSAKEMVGOMKXYSIVSRNCEHFTVTL 120
DB 61 KRERLDGVGGCCYRVNNSLDHEYOPRPEVITISSAKEMVGOMKXYSIVSRNCEHFTVTL 120
QY 121 RYKSRCKQVEKAKVEGVATAGILVAGCSFXIRRYOKKATA 164
DB 121 RYKSRCKQVEKAKVEGVATAGILVAGCSFXIRRYOKKATA 164

RESULT 4
US-08-808-303-12
Sequence 12, Application US/08808303
Patent No. 5776687
GENERAL INFORMATION:
APPLICANT: Nagpal, Sunil
APPLICANT: Disepio, Daniel

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2004, 10:58:15 ; Search time 40 Seconds
(without alignments)
1072.813 Million cell updates/sec

Title: US-10-020-618-1

Perfect score: 852
Sequence: 1 MASHPHEKPGDLIEIFRLG.....ILVVGSGFYIRYQKKA 164

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1065169 seqs, 261661801 residues

Total number of hits satisfying chosen parameters: 1065169

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09C_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	851	99.9	164	US-10-616-942-2	Sequence 2, Appl1
2	851	99.9	164	US-10-616-942-16	Sequence 16, Appl1
3	850	99.8	164	US-10-020-618-1	Sequence 1, Appl1
4	839	98.5	164	US-10-171-911-198	Sequence 198, Appl1
5	423.5	49.7	160	US-10-020-618-4	Sequence 4, Appl1
6	417.5	49.0	162	US-10-616-942-26	Sequence 26, Appl1
7	417.5	49.0	162	US-10-616-942-27	Sequence 27, Appl1
8	417.5	49.0	162	US-10-020-618-3	Sequence 3, Appl1
9	415.5	48.8	169	US-09-925-300-1341	Sequence 1341, Appl1
10	350	41.1	168	US-10-616-942-1	Sequence 1, Appl1
11	350	41.1	168	US-10-616-942-14	Sequence 14, Appl1
12	345	40.5	237	US-09-764-891-3842	Sequence 3842, Appl1
13	135	15.8	82	US-09-764-891-3247	Sequence 3247, Appl1
14	126	14.8	99	US-09-764-891-3660	Sequence 3660, Appl1
15	99.5	11.7	296	US-10-425-114-64719	Sequence 64719, Appl1

16	98	11.5	1738	14	US-10-314-739-2	Sequence 2, Appl1
17	95	11.2	311	12	US-10-425-114-64839	Sequence 64839, A
18	93	10.9	304	12	US-10-425-114-70402	Sequence 70402, A
19	91	10.7	329	12	US-10-425-114-58957	Sequence 58957, A
20	90.5	10.6	259	12	US-10-424-539-142890	Sequence 142890, A
21	90	10.6	201	12	US-10-424-539-168222	Sequence 168222, A
22	87.5	10.3	260	12	US-10-424-539-181930	Sequence 181930, A
23	86.5	10.2	194	12	US-10-425-114-58343	Sequence 58343, A
24	83.5	9.8	337	14	US-10-156-761-13590	Sequence 13590, A
25	83	9.7	358	14	US-10-156-761-11004	Sequence 11004, A
26	80.5	9.4	393	12	US-10-424-539-26247	Sequence 26247, A
27	80	9.4	410	15	US-10-368-493-5975	Sequence 9975, A
28	79.5	9.3	305	12	US-10-425-114-53077	Sequence 53077, A
29	79.5	9.3	319	12	US-10-425-114-71733	Sequence 71733, A
30	79	9.3	141	12	US-10-424-539-181931	Sequence 181931, A
31	79	9.3	278	12	US-10-425-114-61459	Sequence 61459, A
32	76.5	9.0	783	12	US-10-288-1122A-61551	Sequence 61551, A
33	76.5	9.0	857	15	US-10-368-493-10874	Sequence 10874, A
34	76	8.9	363	14	US-10-156-761-11542	Sequence 11542, A
35	75.5	8.9	173	9	US-09-738-626-6015	Sequence 6015, A
36	75.5	8.9	4881	14	US-10-156-761-8481	Sequence 8481, A
37	74.5	8.7	392	12	US-10-425-114-64608	Sequence 64608, A
38	74	8.7	453	15	US-10-369-493-6714	Sequence 6714, A
39	73.5	8.6	398	14	US-10-156-761-11001	Sequence 11001, A
40	73.5	8.6	500	14	US-10-081-051-40	Sequence 40, Appl1
41	73.5	8.6	669	12	US-10-282-122A-73417	Sequence 73417, A
42	73.5	8.6	671	9	US-09-815-242-13864	Sequence 13864, A
43	72.5	8.5	671	12	US-10-282-122A-75582	Sequence 75582, A
44	72.5	8.5	432	15	US-10-369-493-3436	Sequence 3436, A
45	72.5	8.5	836	12	US-10-425-114-51748	Sequence 51748, A

ALIGNMENTS

US-10-616-942-2	RESULT 1
Sequence 2 Application US/10616942	
Publication NO. US20040048339A1	
GENERAL INFORMATION:	
APPLICANT: Kato, Seishi	
TITLE OF INVENTION: Sekine, Shingo	
TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND	
FILE REFERENCE: GIN-6710CPUS	
CURRENT APPLICATION NUMBER: US/10/616,942	
CURRENT FILING DATE: 2003-07-11	
PRIOR APPLICATION NUMBER: US/09/529,100	
PRIOR FILING DATE: 2000-08-21	
PRIOR APPLICATION NUMBER: JP 0276269	
PRIOR FILING DATE: 1997-10-08	
PRIOR APPLICATION NUMBER: PCT/JP98/04474	
PRIOR FILING DATE: 1998-10-05	
NUMBER OF SEQ ID NOS: 28	
SOFTWARE: Patentin Ver. 2.0	
SEQ ID NO 2	
LENGTH: 164	
TYPE: PRT	
ORGANISM: Homo sapiens	
US-10-616-942-2	
Query Match	99.9%; Score 851; DB 12; Length 164;
Best Local Similarity	99.4%; Pred. NO. 1.3e-85;
Matches 163; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
QY	1 MASHPHEKPGDLIEIFRLG.....ILVVGSGFYIRYQKKA 60
DB	1 MASHPHEKPGDLIEIFRLG.....ILVVGSGFYIRYQKKA 60
QY	KEERLEDDVGGCCYRNNSLDEHYQPRPEVITSSAKEMVGGKMYYSYRNCEHFVTL 120
DB	KEERLEDDVGGCCYRNNSLDEHYQPRPEVITSSAKEMVGGKMYYSYRNCEHFVTL 120

QY 121 RYKSRCKQVEKAKVEGVATLALGILVAGCSFYIRRYOKKATA 164
DB 121 RYKSRCKQVEKAKVEGVATLALGILVAGCSFYIRRYOKKATA 164

RESULT 2

US-10-616-942-16
Sequence 16, Application US/10616942
Publication No. US20040048339A1
GENERAL INFORMATION:
APPLICANT: Kato, Seishi
TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND
FILE REFERENCE: GIN-6710CPUS
CURRENT APPLICATION NUMBER: US/10/616, 942
CURRENT FILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: US/09/529,100
PRIOR FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: PCT/JP98/04474
PRIOR FILING DATE: 1997-10-08
PRIOR APPLICATION NUMBER: PCT/JP98/04474
PRIOR FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16
LENGTH: 164
TYPE: PRT
ORGANISM: Homo sapiens
US-10-616-942-16

Query Match 99.9%; Score 851; DB 12; Length 164;
Best Local Similarity 99.4%; Pred. No. 1.3e-85;
Matches 163; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MASHQEPKPGDLIEIFRLGYEHMALYIGDGYVTHLAPSEYFGASSSVFVLSNSAEV 60
DB 1 MASHQEPKPGDLIEIFRLGYEHMALYIGDGYVTHLAPSEYFGASSSVFVLSNSAEV 60
QY 61 KRERLEDVVGCCCVRVNNSLDHEYQPRPVEVISSAKEMWGQKMKYSIVSNCEHFTOL 120
DB 61 KRERLEDVVGCCCVRVNNSLDHEYQPRPVEVISSAKEMWGQKMKYSIVSNCEHFTOL 120
QY 121 RYKSRCKQVEKAKVEGVATLALGILVAGCSFYIRRYOKKATA 164
DB 121 RYKSRCKQVEKAKVEGVATLALGILVAGCSFYIRRYOKKATA 164

RESULT 3

US-10-020-618-1
Sequence 1, Application US/10020618
Publication No. US20020156256A1
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
TITLE OF INVENTION: A NOVEL H-REV107-LIKE
PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/020,618
FILING DATE: 06-Dec-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/801,742
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0200 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-845-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 164 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-020-618-1

Query Match 99.8%; Score 850; DB 13; Length 164;
Best Local Similarity 100.0%; Pred. No. 1.6e-85;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASHQEPKPGDLIEIFRLGYEHMALYIGDGYVTHLAPSEYFGASSSVFVLSNSAEV 60
DB 1 MASHQEPKPGDLIEIFRLGYEHMALYIGDGYVTHLAPSEYFGASSSVFVLSNSAEV 60
QY 61 KRERLEDVVGCCCVRVNNSLDHEYQPRPVEVISSAKEMWGQKMKYSIVSNCEHFTOL 120
DB 61 KRERLEDVVGCCCVRVNNSLDHEYQPRPVEVISSAKEMWGQKMKYSIVSNCEHFTOL 120
QY 121 RYKSRCKQVEKAKVEGVATLALGILVAGCSFYIRRYOKKATA 164
DB 121 RYKSRCKQVEKAKVEGVATLALGILVAGCSFYIRRYOKKATA 164

RESULT 4

US-10-171-311-198
Sequence 198, Application US/10171311
Publication No. US20030087270A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Chen, Yan
APPLICANT: Zhao, Xumei
APPLICANT: Monahan, John
APPLICANT: Kametkar, Shubhangi
APPLICANT: Glatt, Karen
APPLICANT: Gannavarapu, Manjula
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
FILE REFERENCE: MRI-035
CURRENT APPLICATION NUMBER: US/10/171,311
CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US 60/298,159
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/335,936
PRIOR FILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 238
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 198
LENGTH: 164
TYPE: PRT
ORGANISM: Homo sapiens
US-10-171-311-198

Query Match 98.5%; Score 839; DB 14; Length 164;
Best Local Similarity 98.2%; Pred. No. 2.7e-84;
Matches 161; Conservative 0; Mismatches 3; Indels 0; Gaps 0;